

SEQUENCE LISTING

<110> Horton, Holly  
Parker, Suezanne  
Manthorpe, Marston  
Felgner, Philip

<120> Treatment of Cancer Using Cytokine-Expressing  
Polynucleotides and Compositions Therefor

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<151> 1997-11-20

<150> US 60/079,914

<151> 1998-03-30

<150> US 60/100,820

<151> 1998-09-15

<150> US 09/196,313

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<170> PatentIn Ver. 2.0

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Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
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ctt agc agg aac acc ttg gtg ctt ctg cac caa atg agg aga atc tcc 144  
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
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cct ttc ttg tgt ctc aag gac aga aga gac ttc agg ttc ccc cag gag 192  
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
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atg gta aaa ggg agc cag ttg cag aag gcc cat gtc atg tct gtc ctc 240  
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
45 50 55

cat gag atg ctg cag cag atc ttc agc ctc ttc cac aca gag cgc tcc 288  
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser

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tct gct gcc tgg aac atg acc ctc cta gac caa ctc cac act gga ctt			336
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu			
75	80	85	
cat cag caa ctg caa cac ctg gag acc tgc ttg ctg cag gta gtg gga			384
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly			
90	95	100	105
gaa gga gaa tct gct ggg gca att agc agc cct gca ctg acc ttg agg			432
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg			
110	115	120	
agg tac ttc cag gga atc cgt gtc tac ctg aaa gag aag aaa tac agc			480
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser			
125	130	135	
gac tgt gcc tgg gaa gtt gtc aga atg gaa atc atg aaa tcc ttg ttc			528
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe			
140	145	150	
tta tca aca aac atg caa gaa aga ctg aga agt aaa gat aga gac ctg			576
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Gly Ser Ser			
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Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser			
10	15	20	25
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu			
30	35	40	
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu			
45	50	55	



His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
60 65 70

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
75 80 85

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
90 95 100 105

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
110 115 120

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
125 130 135

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
140 145 150

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
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Gly Ser Ser  
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Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Glu Thr His Ser Leu  
-5 -1 1 5

gat aac agg agg acc ttg atg ctc ctg gca caa atg agc aga atc tct 144

Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Glu Thr His Ser Leu  
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Pro	Ser	Ser	Cys	Leu	Met	Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu
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Glu	Phe	Asp	Gly	Asn	Gln	Phe	Gln	Lys	Ala	Pro	Ala	Ile	Ser	Val	Leu
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Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys	Val	Met	Gln	Glu	Glu	Arg
90				95						100					105
Val	Gly	Glu	Thr	Pro	Leu	Met	Asn	Ala	Asp	Ser	Ile	Leu	Ala	Val	Lys
				110					115					120	
Lys	Tyr	Phe	Arg	Arg	Ile	Thr	Leu	Tyr	Leu	Thr	Glu	Lys	Lys	Tyr	Ser
			125				130						135		
Pro	Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Leu	Ser
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Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu	
-5 -1 1 5	
agg aac aag aga gcc ttg aca ctc ctg gta caa atg agg aga ctc tcc	144
Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser	
10 15 20 25	
cct ctc tcc tgc ctg aag gac agg aag gac ttt gga ttc ccg cag gag	192
Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu	
30 35 40	
aag gtg gat gcc cag cag atc aag aag gct caa gcc atc cct gtc ctg	240
Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu	
45 50 55	
agt gag ctg acc cag cag atc ctg aac atc ttc aca tca aag gac tca	288
Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser	
60 65 70	
tct gct gct tgg aat gca acc ctc cta gac tca ttc tgc aat gac ctc	336
Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu	
75 80 85	
cac cag cag ctc aat gac ctg caa ggt tgt ctg atg cag cag gtg ggg	384
His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly	
90 95 100 105	
gtg cag gaa ttt ccc ctg acc cag gaa gat gcc ctg ctg gct gtg agg	432
Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg	
110 115 120	
aaa tac ttc cac agg atc act gtg tac ctg aga gag aag aaa cac agc	480
Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser	
125 130 135	
ccc tgt gcc tgg gag gtg gtc aga gca gaa gtc tgg aga gcc ctg tct	528
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser	
140 145 150	
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<213> Mus musculus

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Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser  
10 15 20 25

Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu  
30 35 40

Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu  
45 50 55

Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser  
60 65 70

Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu  
75 80 85

His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly  
90 95 100 105

Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg  
110 115 120

Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser  
125 130 135

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser  
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Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys  
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Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu	
-1 1 5 10	
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Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile	
15 20 25	
aat aat tac aag aat ccc aaa ctc acc agg atg ctc aca ttt aag ttt	192
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe	
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tac atg ccc aag aag gcc aca gaa ctg aaa cat ctt cag tgt cta gaa	240
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu	
45 50 55 60	
gaa gaa ctc aaa cct ctg gag gaa gtg cta aat tta gct caa agc aaa	288
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys	
65 70 75	
aac ttt cac tta aga ccc agg gac tta atc agc aat atc aac gta ata	336
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile	
80 85 90	
gtt ctg gaa cta aag gga tct gaa aca aca ttc atg tgt gaa tat gct	384
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala	
95 100 105	
gat gag aca gca acc att gta gaa ttt ctg aac aga tgg att acc ttt	432
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe	
110 115 120	
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Cys Gln Ser Ile Ile Ser Thr Leu Thr	
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<211> 153

<212> PRT

<213> Homo sapiens

<400> 14

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Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile  
15 20 25

Asn Asn Tyr Lys Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe  
30 35 40

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu  
45 50 55 60

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys  
65 70 75

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile  
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